

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 207

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAGCAGCA ATCCTAAACC TCAAGAAAA ACCAAGCGTA ACACCAACCG CCGCCCTCAK	60
GGSGTNNNNN NNCCGGGTGG CGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG	120
GGCCCCAGGN NGGGTGTGCG CGCGACTAGG AAGACTTCCG AGCGGTACAA ACCTCGTGCC	180
AGGCGACAGC CTATCCCCAA GGCTCGYCGG YCCGAGGGCA GGTCCTGGGC TCAGCCCGGG	240
TATCCTTGGC CCCTCTATGG CAATGAGGGC TCGGGGTGGG CGGGNIGGCT CCGTCCCCC	300
CGCGGCTCTC GGCCCAATTG GGGCCCC	327

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	1	5	10	15
Arg Arg Pro Xaa Xaa Xaa Xaa Xaa Pro Gly Gly Gly Gln Ile Val Gly	20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Xaa Gly Val Arg Ala	35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	50	55	60	
Ile Pro Lys Ala Xaa Arg Xaa Glu Gly Arg Ser Trp Ala Gln Pro Gly	65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp	85	90	95	
Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro	100	105		

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GACGGCGTGA ACTATGCAAC AGGGAACITG CCCGGTIGCT CTTCTCTAT CTTCTCTTG 60
 GCTTTGCTGT CTGCTTGAC GGTTCACAC ACCGCTCAGG AGGTGCCCAA CGCATCCGGG 120
 GTGTATCATG TCACCAACGA CTGTTCCAC TCGAGCATCA TCTATGAGAT GGACGGTATG 180
 ATCATGCACT ACCCAGGGTG CTGCCCCCTG GTTCGGGAGG ATAACCATCT CCGCTGCTGG 240
 ATGGCGCTCA CCCCCACGCT TCGGGTCAAA AAYGCTAGTG TCCCCACTRC GGCAATCCGA 300
 CGTCACGTCG ACTTGCTTGT TGGGGGNNCC ACCTTCTGTT CCGTATGTA CGTGGGRCAC 360
 CTTTGGGGGT CTGTCTTCTT CGCTGGCCAG CTATTCACCT TTTACCCCG CATGCACCAT 420
 ACAACGCAGG AGTGCAACTG CTCAATC 447

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
 1 5 10 15
 Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Xaa Thr Ala
 20 25 30
 His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp Cys
 35 40 45
 Ser Asn Ser Ser Ile Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr
 50 55 60
 Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn His Leu Arg Cys Trp
 65 70 75 80
 Met Ala Leu Thr Pro Thr Leu Ala Val Lys Xaa Ala Ser Val Pro Thr
 85 90 95
 Xaa Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Xaa Xaa Thr Phe
 100 105 110
 Cys Ser Ala Met Tyr Val Xaa Asp Leu Cys Gly Ser Val Phe Leu Ala
 115 120 125
 Gly Gln Leu Phe Thr Phe Ser Pro Arg Met His His Thr Thr Gln Glu
 130 135 140
 Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGAGCACGA ATCTAAACC TCAAGAAAA ACCAAACGTA ACACCAACCG CCGCCACAG	60
GACGTCAAGN TOCCGGGTGG TGCTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCCCAGG	120
GGCCCCAGGT TGGGTGTGGC CGCGACCRGG AAGACTTCGG AGCGGTGCA GCCTCGTGAC	180
AGCGGACAGC CTATTCCTAA GGCTCGCCAG TCCGATGGCA GNNCCTGGGC TCAGCCAGGG	240
CATCCCTGGC CCCTCTATGG CAATGAGGGC TCGGATGGG CGGGATGGCT CCTGTCCCCC	300
CCCGGCTCTC GGCCCAATTG GGGCCCC	327

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	1 5 10 15
Arg Arg Pro Gln Asp Val Lys Xaa Pro Gly Gly Gly Gln Ile Val Gly	20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	35 40 45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Asp Arg Arg Gln Pro	50 55 60
Ile Pro Lys Ala Arg Gln Ser Asp Gly Xaa Xaa Trp Ala Gln Pro Gly	65 70 75 80
His Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	85 90 95
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro	100 105

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GACGGCGTGA ACTATGCAAC AGGGAATTTG CCTGGTTGCT CTTTCTCTAT CTTCTCTTA	60
GCTTTCTGCT CCGCTTTCAC GGTCCAACCT ACCGCTCATG AGTGCGCAA CGCATCCGGG	120
GTATATCATC TCACCAATGA CTGTCCAAC TCGAGCATCA TCTATGAGAT GAGTGGIATG	180

ATCTTGACAG CCCAGGGTG TGTGCCCTGC GTTCGGGAGA ACAACTCTTC TCGTTGCTGG 240
 ATGCCRCCTCA CCCCCACGCT TCGGGTCAAA GACGCTAATG TCCCTACTGC GGCAATCCGA 300
 CGCCATGTGG ACTTGCTGGT TGGGACAGCC GCGTTTCGTT CCGCTATGTA CGTGGGGGAC 360
 CTCTGCGGAT CCGTCTTCT TGTGGGCCAG CTATTCACCT TTTCACCCCG CTGTACCAT 420
 ACAACACAGG AGTGCAACTG CTCATC 447

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
 1 5 10 15
 Ile Phe Leu Leu Ala Phe Leu Ser Cys Leu Thr Val Pro Thr Thr Ala
 20 25 30
 His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu Thr Asn Asp Cys
 35 40 45
 Ser Asn Ser Ser Ile Ile Tyr Glu Met Ser Gly Met Ile Leu His Ala
 50 55 60
 Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp
 65 70 75 80
 Met Xaa Leu Thr Pro Thr Leu Ala Val Lys Asp Ala Asn Val Pro Thr
 85 90 95
 Ala Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Thr Ala Ala Phe
 100 105 110
 Arg Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val
 115 120 125
 Gly Gln Leu Phe Thr Phe Ser Pro Arg Leu Tyr His Thr Thr Gln Glu
 130 135 140
 Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGAGCACGA ATCTAAACC TCAAAGAAA ACCAAAAGAA ACACCAACCG CCGCCACAG 60
 GACGTCAGT TCCCGGCGG TCGCCAGATC GTTCGTGGAG TCTACGTGCT ACCGCCAGG 120
 GGCCCTAGAT TGGGTGTGGC CGCAGCCCGG AAGACTTCGG AGCGGTGCGA ACCTCGTGGG 180
 AGCGGCCAAC CTATTCCCAA GGAGCCCGCA CCCGAGGCCA GGT 223

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Ala Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Glu Arg Arg Pro Glu Gly Arg
 65 70

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 957 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGAGCAGCA ATCTTAAC TCAGAGAAA ACCAAACGCA ACACCAACCG CCGCCCAAG 60
 CACGTTAAAT TCCCGGGTGG GGGGCAGATC GTGGGTGGAG TTTACTTGTT GCCGCTCAGG 120
 GGCCCCAGGT TGGGTGTGGC CGGCACGAGG AAGACTTCGG AGCGGTGCGA ACCTGCGGGA 180
 AGCGACAGC CTATCCCAA GGCTCGCCGA CCCGAGGGCA GGTCTGGGC TCAGCTGGG 240
 TACCATGGC CCTCTATGC TAACGAGGGC TCGGATGGG CGGGATGGCT CTTGTCCCT 300
 CCGGCTCCG CTCCTAGCTG GGGCCCCAAT GACCCCGAC GTAGATCAG CAATTGGGT 360
 AAGGTCATCG ATACCCTAAC GTGTGGCTTC GCCGATCTCA TGGGTACAT TCCGCTCGTC 420
 GCGCCCCCG TAGGGGGCGC TTCCAGAACC CTGNCACATG GTGTCCGGT CTTGGNAGGC 480
 GCGGTGATNN NNNNNNNNN NAACCTTCN GGTGTCTCTT TNNCTATCTT CTTCTTGGCN 540
 TTACTCTCTT GCCTCAGAT CCCACCTCT GCCTATGAGG TGCACAGCAC AACCGATGGC 600
 TACCATGTCA CTAATGACTG TTCCAACGGC AGCATCGTAT ATGAGGCAAA GGACATCATC 660
 CTTACACGC CTGGGTGNGT GCCCTGCATA CGGGAAGGCA ATATCTCCCG TTGCTGGGTA 720
 CCGCTCACCC CCACGCTCGC AGCGCGGATC GCGAACGCTC CATCGATGA GGTGCGCGCT 780
 CACGTCGACC TCCTCGTGGG GGCAGCGGTG TCTGTCTCAG CCATGTACAT TGGGGACCTT 840
 TGTGGGGGCG TCTTCTCTGT TGGGCAATTG TTCACCTTCA CGTCCCGGCG GCATTGGACG 900
 GTGCAGGACT GTAATTGTTT CATTACTCTT GGCCACATAA CGGGCCACCG NNNNNNN 957

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60
Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly
65 70 75 80
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
130 135 140
Gly Gly Ala Ser Arg Thr Leu Xaa His Gly Val Arg Val Leu Xaa Gly
145 150 155 160
Gly Val Xaa Xaa Xaa Xaa Xaa Asn Leu Xaa Gly Cys Ser Xaa Xaa Ile
165 170 175
Phe Leu Leu Xaa Leu Leu Ser Cys Leu Thr Val Pro Thr Ser Ala Tyr
180 185 190
Glu Val His Ser Thr Thr Asp Gly Tyr His Val Thr Asn Asp Cys Ser
195 200 205
Asn Gly Ser Ile Val Tyr Glu Ala Lys Asp Ile Ile Leu His Thr Pro
210 215 220
Gly Xaa Val Pro Cys Ile Arg Glu Gly Asn Ile Ser Arg Cys Trp Val
225 230 235 240
Pro Leu Thr Pro Thr Leu Ala Ala Arg Ile Ala Asn Ala Pro Ile Asp
245 250 255
Glu Val Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Val Phe Cys
260 265 270
Ser Ala Met Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu Val Gly
275 280 285
Gln Leu Phe Thr Phe Thr Ser Arg Arg His Trp Thr Val Gln Asp Cys
290 295 300
Asn Cys Ser Ile Tyr Ser Gly His Ile Thr Gly His Xaa Xaa Xaa
305 310 315

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

106050"88F5860

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATGAGCACAA ATCCTAAACC TCAAAGAAA ACCAAAGAA ATACCAACCG CCGCCCACAG	60
GACGTCAAGT TCCCGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGTI GCCGCGCAGG	120
GGCCCCAGAT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCACGTGGA	180
AGGCGCCAGC CCATCCCTAA AGATCGGNGN GCCACTGGCA GGTCTTGGG ACGTCCAGGA	240
TATCCCTGCC CCTGTATGG GAACGAGGGG CTCGGCTGGG CAGGATGCTT CCTGTCCCC	300
CGAGGCTCTC	310

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	1	5	10	15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	50	55	60	
Ile Pro Lys Asp Arg Xaa Ala Thr Gly Arg Ser Trp Gly Arg Pro Gly	65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp	85	90	95	
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly	100	105		

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACGTCCGGNT NTGCCGACCT CATGGGTAC ATNCCCGTTG TCGGGGCCCC GGTGGGCGGG	60
GINGCCAGGG CCTTCGCGNA TGGCGTGCGG GTCTGGAGG ACGGGATAAA TTATGNAACA	120
GGGAACCTCC CTGGTGTCTC CTTTCTATC TTCTNGTTGG CTCTTCTGTC TTGTGTACCC	180
GTGCTGTCT CTGNCGTIGA GGTCAAAAT ACCAGTCAGG CCTATAAGGC AACCAACGAC	240
TGCTCCAACA ACAGCATCGT ATGCCAATTG GNGGACGGGG TGCTTCATGT TCCTGGATGT	300
GTCCCCTGCG AGAATAGCTC CGGTGGGTTC CACTGTGTGA TCCCGAICTC GCCCAACATA	360

GCCGTGAGCA AACCTGGTGC TCTACCAAG GGA CTGCGGG CACGCATTGA TGCCGTCGTG 420
ATGTCGGCCA CCTCTGCTC TGCCCTGTAC GTGGGAGATG TGTGCGGGC ACTGATGATA 480
GCTGCACAGG CTTTCATCGT GGCACCGAAG CGCCATTACT TCGTCCAGGA ATGCAATTGC 540
TCCATATACC CAGGCCACAT TACAGGTCAT CGCATGGCG 579

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Thr Cys Xaa Xaa Ala Asp Leu Met Gly Tyr Xaa Pro Val Val Gly Ala
1 5 10 15
Pro Val Gly Gly Xaa Ala Arg Ala Leu Ala Xaa Gly Val Arg Val Leu
20 25 30
Glu Asp Gly Ile Asn Tyr Xaa Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45
Ser Ile Phe Xaa Leu Ala Leu Leu Ser Cys Val Thr Val Pro Val Ser
50 55 60
Xaa Val Glu Val Lys Asn Thr Ser Gln Ala Tyr Met Ala Thr Asn Asp
65 70 75 80
Cys Ser Asn Asn Ser Ile Val Trp Gln Leu Xaa Asp Ala Val Leu His
85 90 95
Val Pro Gly Cys Val Pro Cys Glu Asn Ser Ser Gly Arg Phe His Cys
100 105 110
Trp Ile Pro Ile Ser Pro Asn Ile Ala Val Ser Lys Pro Gly Ala Leu
115 120 125
Thr Lys Gly Leu Arg Ala Arg Ile Asp Ala Val Val Met Ser Ala Thr
130 135 140
Leu Cys Ser Ala Leu Tyr Val Gly Asp Val Cys Gly Ala Val Met Ile
145 150 155 160
Ala Ala Gln Ala Phe Ile Val Ala Pro Lys Arg His Tyr Phe Val Gln
165 170 175
Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGAGCACAA ATCTAAACC TCAAAGAAA ACTAAAGAA AACTAACC GCGCCACAG 60
GACGTTAAGT TCCCGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGT GCCCGCAGG 120

GGCCCCAGGT	TGGGTGTGCG	CGCGCCAAGG	AAGACTTCTG	AACGGTCCCA	GCCACGTGGA	180
AGGCGCCAGC	CCATCCCAA	AGATCGCGCG	GCCACTGGCA	AGTCCTGGGG	ACGTCCAGGA	240
TACCCTTGGC	CCCTGTACGG	GAACGAGGGC	CTCGGTGGGG	CAGGGTGGCT	CCTGTCCCCC	300
CGGGGCTCTC	GCCCTCGTGT	GGGCCCCAAC	GACCCCGCGG	ACAGGTCACG	CAACTTGGGT	360
AAGGTCATCG	ATACCCCTCAC	GTGTGGCTTT	GSCGACCTCA	TGGGGTACAT	ACCTGTCTGC	420
GGCGCCCTG	TGGCGCGCGT	TGCCAGAGCC	CTCGCGCATG	GCGTGCGGGT	CCTGGAGGAC	480
GGGATAAAAT	ATGCAACAGG	GAACCTGCCC	GGTGTGCTCT	TTTCTATCTT	CTTGCTGGCT	540
CTCTTGCTTT	GTATCACCGT	GCCCGTGCTC	GCCATACAGG	TAAAGAACA	CAGCCACTTC	600
TACATGGCGA	CTAATGACTG	TGCCAATGAC	AGCATCGTCT	GGCAGCTCAG	GGACGCGGTG	660
CTCCATGTTT	CTGGATGTGT	CCCTGTGTAG	AGGTCAGGTA	ATAGGACCTT	CTGTTGGACA	720
GCGGTCTCCG	CCAACGTGGC	TGTGAGCCGA	CCTGGTGTCT	TCACTAGAGG	TCTGCGGGCT	780
CACATTGATA	CCATCGTGAT	GTCCGCCACC	CTCTGCTCTG	CCCTATACAT	AGGGGACCTA	840
TGCGGCGCTG	TGATGATAGC	AGCGCAAGTT	GCCGTGCTCT	CACCGCAATA	CCATACTTTT	900
GTCCAGGAAT	GCAACTGCTC	CATATACCCA	GGCCATATCA	CAGGACATCG	AATGGNN	957

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Ser	Thr		Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5						10					15	
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gly	Gln	Ile	Val	Gly
			20					25						30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	
		35					40					45				
Pro	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	
		50				55						60				
Ile	Pro	Lys	Asp	Arg	Arg	Ala	Thr	Gly	Lys	Ser	Trp	Gly	Arg	Pro	Gly	
65				70					75						80	
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	
			85					90						95		
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro	
			100					105					110			
Arg	His	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	
			115				120						125			
Gly	Phe	Xaa	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val	Gly	Ala	Pro	Val	
			130			135					140					
Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	Hic	Gly	Val	Arg	Val	Leu	Glu	Asp	
145				150						155				160		
Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	
			165					170						175		
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Ile	Thr	Val	Pro	Val	Ser	Ala	Ile	
			180					185					190			
Gln	Val	Lys	Asn	Asn	Ser	His	Phe	Tyr	Met	Ala	Thr	Asn	Asp	Cys	Ala	
		195				200						205				

005138.050901

Asn Asp Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro
210 215 220
Gly Cys Val Pro Cys Glu Arg Ser Gly Asn Arg Thr Phe Cys Trp Thr
225 230 235 240
Ala Val Ser Pro Asn Val Ala Val Ser Arg Pro Gly Ala Leu Thr Arg
245 250 255
Gly Leu Arg Ala His Ile Asp Thr Ile Val Met Ser Ala Thr Leu Cys
260 265 270
Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Ile Ala Ala
275 280 285
Gln Val Ala Val Val Ser Pro Gln Tyr His Thr Phe Val Gln Glu Cys
290 295 300
Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Xaa
305 310 315

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GACGGGGTAA ATTATGCAAC AGGGAATCTG CCTGGTTGCT CTTCTCTAT CTTCTTGTG 60
GCTCTTCTGT CTGTGTCTAC CGTGCCTGTC TCTGCCGTGC AGGTTAAGAA CACCACTACC 120
ATGTACATGG CAACCAATGA CTGTTCCAAAC AACAGCATCA TCTGGCAAAT GCAGGCGCGG 180
GTGCTTCATG TTCCTGGATG TGTCCCGTGT GAGTTGCAGG GCAATAAGTC CCGGTGCTGG 240
ATACCGGTCA CTCCCAACGT GGCTGTGAAC CAGCCCGCGG CCCTCACTAG GGGCTTGCGG 300
ACGCACATGG ACACCATCGT GATGGTCGCT ACGCTCTGTT CTGCACTCTA CATCGGGGAC 360
GTGTGTGGCG CGGTGATGAT AGCTGCTCAG GTTGTCAATG TCTGCGCGCA ACATCACAAC 420
TTTTCGCCAG ATTGCAATTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Val Thr Val Pro Val Ser Ala
20 25 30
Val Gln Val Lys Asn Thr Ser Thr Met Tyr Met Ala Thr Asn Asp Cys
35 40 45
Ser Asn Asn Ser Ile Ile Trp Gln Met Gln Gly Ala Val Leu His Val
50 55 60

Pro Gly Cys Val Pro Cys Glu Leu Gln Gly Asn Lys Ser Arg Cys Trp
65 70 75 80

Ile Pro Val Thr Pro Asn Val Ala Val Asn Gln Pro Gly Ala Leu Thr
85 90 95

Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Met Val Ala Thr Leu
100 105 110

Cys Ser Ala Leu Tyr Ile Gly Asp Val Cys Gly Ala Val Met Ile Ala
115 120 125

Ala Gln Val Val Ile Val Ser Pro Gln His His Asn Phe Ser Gln Asp
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATGAGCACAA ATCTTAACCC TCAAAGAAAA ACCAAAGAA AACTAACCG CCGCCACAG 60
GACGTAACT TCCCGGGCGG TGGCCAGATC GTTGGCGGAG TATACTTGT GCCGCCAGG 120
GGCCCCCGGT TGGGTGTGGC CGCGACGAGG AAAACTTCCG AACGGTCCA GCCACGTGG 180
AGGCCCCAGC CCATCCCTAA AGATCGGCGC TCCACTGGCA AATCCTGGG ACGTCAGGA 240
TACCCTTGGC CCTGTATGG GAACGAGGGC CTTGGTTGG CAGGATGGCT CTGTCCCT 300
CGAGGCTCTC 310

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Arg Ser Leu Ala
20 25 30

Glu Tyr Thr Cys Ala Arg Arg Gly Lys Leu Arg Arg Ser Ser Met Gly
35 40 45

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

GACGGGATAA ACTACGCAAC AGGGAATCTG CCCGGTTGCT CCTTTCTAT CTTCCTGCTG      60
GCCTTGCTAT CCTGTCTCAC TGTGCGGCGG TCCGCTGTGC AGGTCAAGAA CACCAGCCAC      120
TCTTATATGG TGACCAATGA TTGCTCAAAC AGCAGCATTG TCTGGCAGCT TAAGGATGCT      180
GTGCTTCACG TCCCTGGATG TGTTCATGT GAGAGGCACC AAAATCAGTC TCGCTGCTGG      240
ATACCTGTGA CACCAATGT GGCCTGAGC CAACCTGGCG CGCTCACCAG GGGTTTGGCG      300
ACGCACATGG ACACCATCGT TCGCTCTGCT ACCGTCTGCT CAGCTTGTGA TGTGGGCGAC      360
TTCTGCGGCG CAGTGATGTT GGTCTCTCAA TTTTCATGA TCTCCCTCA GCACCACATC      420
TTCGTCCAGG AITGCAACTG CTCGATA                                           447

```

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1           5           10           15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20          25          30
Val Gln Val Lys Asn Thr Ser His Ser Tyr Met Val Thr Asn Asp Cys
35          40          45
Ser Asn Ser Ser Ile Val Trp Gln Leu Lys Asp Ala Val Leu His Val
50          55          60
Pro Gly Cys Val Pro Cys Glu Arg His Gln Asn Gln Ser Arg Cys Trp
65          70          75          80
Ile Pro Val Thr Pro Asn Val Ala Val Ser Gln Pro Gly Ala Leu Thr
85          90          95
Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Ala Ser Ala Thr Val
100         105         110
Cys Ser Ala Leu Tyr Val Gly Asp Phe Cys Gly Ala Val Met Leu Val
115         120         125
Ser Gln Phe Phe Met Ile Ser Pro Gln His His Ile Phe Val Gln Asp
130         135         140
Cys Asn Cys Ser Ile
145

```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GACGGGATAA ACTATGCAAC AGGGAACCTG CCTGGTTGCT CCTTTCTAT CTCTTACTG	60
GCCCTGCTTT CTTCATCAC CGTGCCGGTC TCTGCCGTGC AAGTTGCGAA CCGCAGTGGT	120
TCTTACATGG TGACCAATGA TTGCTCGAAC AGCAGCATCG TTTGGCAGCT CGAGGAGGCC	180
GTCCTTCACG TCCCTGGATG TGTTCCCTGT GAGTGAAGG ACRACACCTC CCGCTGCTGG	240
ATACCGGTCA CCCCTAACAT CGCTGTGAGC CAACCTGGCG CGCTTACCAA GGGCCTGCGG	300
ACACATAITG ACATCATTGT CGCGTCCGCC ACGTCTGCT CTGCCTIGTA TGTGGG	356

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	1	5	10	15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Ala	20	25	30	
Val Gln Val Ala Asn Arg Ser Gly Ser Tyr Met Val Thr Asn Asp Cys	35	40	45	
Ser Asn Ser Ser Ile Val Trp Gln Leu Glu Glu Ala Val Leu His Val	50	55	60	
Pro Gly Cys Val Pro Cys Glu Trp Lys Asp Asn Thr Ser Arg Cys Trp	65	70	75	80
Ile Pro Val Thr Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Xaa Thr	85	90	95	
Lys Gly Leu Arg Thr His Ile Asp Ile Ile Val Ala Ser Ala Thr Phe	100	105	110	
Cys Ser Ala Leu Tyr Val	115			

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATGAGCACGA ATCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CGGCCCATG	60
GACGTTAAGT TCCCGGGTGG TGGCCAGATC GTTGGCGGAG TTTACTTGTG GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTGGG AGCGGTCCGA ACCTCGTGGG	180
AGAGCCCAAC CTATCCCAAA GGC CGCTCGA TCCGAGGAA GGTCTGGGC ACAGCCAGGA	240
TATCCATGGC CTCTTACGG TAATGAGGGT TCGGGTGGG CANNATGGCT CTGTCCCCC	300
CGCGGTTCTC	310

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
 35 40 45
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
 Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg
 115

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GACGGGATCA ATTTTGCAAC AGGGAACCTC CCCGGTTGCT CCTTTTCTAT CTTCCTCTTG 60
 GCACTCCTCT CGTGCCCTGAC TGTCCCGCT TCGGCCATCA ACTATCGCAA TGTCTCGGGC 120
 ATTTACTATG TCACCAATGA TTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC 180
 ATCTTGACCC TCCAGGTTG CGTGCCCTGC GTGAGAGAGG GGAATCAGTC ACGTTGCTGG 240
 GTAGCCCTTA CCCCTACCGT CGCAGCGCCA TACATCGGCG CGCCACTTGA GTCTCTACGG 300
 AGTCATGTGG ACTTGATGGT GGGGCGCGCC ACTGTTTGT CAGCCCTTTA CATCGGGGAT 360
 TTGTGTGGYG GCTTGTTCTCT AGTCGGTCAG ATGTTCTCTT TCCGACCAAG GCGCCACTGG 420
 ACTACTCAAG ATTGCAATTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30
Ile Asn Tyr Arg Asn Val Ser Gly Ile Tyr Tyr Val Thr Asn Asp Cys
35 40 45
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50 55 60
Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser Arg Cys Trp
65 70 75 80
Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95
Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
100 105 110
Cys Ser Ala Leu Tyr Ile Gly Asp Xaa Cys Xaa Gly Leu Phe Leu Val
115 120 125
Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp
130 135 140
Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GACGGGATCA ATTATGCAAC AGGGAACCTT CCGGGTTGCT CTTTTCTAT CTTCCTCTTG 60
GCACCTCTCT CGTGCCCTGAC TGTTCGGCT TCGGCCATTA ACTACCGCAA CACCTCGGGC 120
ATCTACCACG TCACCAATGA CTGCCCCGAAC TCGAGCATAG TTTATGAGGC CGACCACCAC 180
ATCTTGACCC TTCCAGGTTG CGTGCCCTCC GTGAGAACTG GGAATCAGTC ACGTTGCTGG 240
GTGGCCCTTA CTCCTACCGT CGCAGCGCCA TACATCGGCG CACCGCTTGA GTCTCTGCGG 300
AGTCATGTGG ATCTGATGGT GGGGGGTGCC ACTGTTTGCT CAGCCCTTTA CATCGGGGAT 360
TTGTGTGGCG GCTTGTCTTT GGTGGTCAG ATGTTTCTT TCCGACCACG ACGCCACTGG 420
ACTGCCCAGG ATTGCAATTG TTCTATC 447

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30

Ile Asn Tyr Arg Asn Thr Ser Gly Ile Tyr His Val Thr Asn Asp Cys
35 40 45

Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50 55 60

Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys Trp
65 70 75 80

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
100 105 110

Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu Val
115 120 125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Ala Gln Asp
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GACGGGATTA ATTATGCAAC AGGGAATCTT CCCGGTTGCT CCTTTCTAT CTTCCCTCTG 60

GCACCTTCTCT CGTGCCCTGAC TGTCCCGCTT TCGGCCATTA ACTACACAA CACCTCGGGC 120

ATCTATCATA TCACCAACGA CTGCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC 180

ATCTGCATC TCCCAGGTTG CGTGCCCTGC GTGAGAGTGG GGAATCAGTC GAGTTGCTGG 240

GTGGCCCTTA CCCCTACCAT CGCAGCGCCA TACATCGGCG CACCGCTTGA GTCCTTGCGG 300

AGTCATGTGG ATCTGATGGT GGGGGCGGCC ACTGTCTGTT CAGCCCTTTA CATCGGGGAT 360

TTGTGTGGCG GTGCGTCTTT GGTGGGTCAG ATGTTCTCTT TCCGACCACG GCGCCACTGG 420

ACCACCCAAG ATTGCAACTG CTCATC 447

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30

0985138-050901

Ile Asn Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp Cys
35 40 45
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50 55 60
Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Ser Cys Trp
65 70 75 80
Val Ala Leu Thr Pro Thr Ile Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95
Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
100 105 110
Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ala Phe Leu Val
115 120 125
Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp
130 135 140
Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GACGGGATCA ATTATGCAAC AGGGAATATT CCCGGTTGCT CYTTTCTAT CTTCCCTTYTG	60
GCACCTTCTCT CGTGTCTGAC TGTCCCGCT TCGGCCACTA ACTATCGCAA CGTCTCGGGC	120
ATCTACCATG TCACCAATGA CTGCCCGAAT TCAAGCATAG TGTATCAGGC CGACCATCAC	180
ATCTTAGCAC TTCCAGGTTG CGTGCCCTGC GTGAGAGTGG GGAACAGTC ACGCTGCTGG	240
GTGGCCCTTA CCCCTACCGT CGCAGCGCCA TACACCGCGG CGCCGCTTGA GTCCCTGCGG	300
AGTCATGTGG ATCTGATGCT GGGAGCTGCC ACTGTTTGT CAGCCCTTTA CATCGGGGAY	360
TTGTGTGGCG GCTTGTCTTT GGTGTGTCAG ATGTTCTCTT TYCAGCCTCG GCGCCACTGG	420
ACTACCCAGG ATTGCAATTG TTCCATC	447

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Ile Pro Gly Cys Xaa Phe Ser	1 5 10 15
Ile Phe Leu Xaa Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	20 25 30
Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys	35 40 45
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu Ala Leu	

50 55 60
 Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys Trp
 65 70 75 80
 Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Thr Ala Ala Pro Leu
 85 90 95
 Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
 100 105 110
 Cys Ser Ala Leu Tyr Ile Gly Xaa Leu Cys Gly Gly Leu Phe Leu Val
 115 120 125
 Gly Gln Met Phe Ser Xaa Gln Pro Arg Arg His Trp Thr Thr Gln Asp
 130 135 140
 Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GACGGGATTA ATTATGCAAC AGGGAAYCTC CCCGGTTCCT CTTTCTCTAT CTCCTCTTG 60
 GCATTCTCT CGTGCTGAC TGTCCCGCT TCGGCCACCA ACTACCGCAA TGTCGGGGC 120
 ATTACCATG TCACCAATGA CTGCCGAAT TCAAGCATAG TGTTCGAGG CGACCATCAC 180
 ATCTTGACCC TTCCAGGATG CGTGCCCTGC GTGAAAGAGG GAAATCATC ACGCTGCTGG 240
 GTGGCCCTTA CCCCTACCGT CGCAGGCCCA TACATCGGCG CGCCACTTGA GTCTCTACGG 300
 AGTCATGTGG ATGTGATGGT GGGGGCTGCC ACTGTTTGT CAGCCCTTTC CATCGGGGAT 360
 CTGTCCGGTG GCTTGTCTCT GGTTCGTCAG ATGTTCTCT TCCGACCACG GCGCCACTGG 420
 ACTACCCAGG AATGCAATTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Asp Gly Ile Asn Tyr Ala Thr Gly Xaa Leu Pro Gly Cys Ser Phe Ser
 1 5 10 15
 Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
 20 25 30
 Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
 35 40 45
 Pro Asn Ser Ser Ile Val Phe Glu Ala Asp His His Ile Leu His Leu
 50 55 60
 Pro Gly Cys Val Pro Cys Val Lys Glu Gly Asn His Ser Arg Cys Trp
 65 70 75 80

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85 90 95
Glu Ser Leu Arg Ser His Val Asp Val Met Val Gly Ala Ala Thr Val
100 105 110
Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu Val
115 120 125
Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Glu
130 135 140
Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GACGGGATCA ATTATGCAAC AGGGAACCTC CCCGGTTGCT CTTCTCTAT CTTTCATCCTG 60
GCACCTCTCT CGTGCTGAC TGTCCCGGCC TCGGCTCAGC ATTATCGGAA TGTCTCGGGC 120
ATTATACCAGC TCACCAACGA CTGCCCGAAC TCCAGCATAG TGTATGAGTC CGACCATCAC 180
ATCTTACACC TACCAGGGTG TGTACCCTGT GTGAAGACTG GGAACACTTC GCGCTGCTGG 240
GTGGCCTTAA CACCTACCGT GCGCCGCGCC ATACTTTCCG CTCCACTTAT GTCCGTACCG 300
CGGCATGTGG ATCTGATGGT GGGTGCAGCT ACCCTATCGT CTGCCCTCTA CGTGGAGAC 360
CTCTGCGGGG GTGCCTTCTT ACTGGGGCAG ATGTTACCT TCCAGCCCGG TCGCCACTCG 420
ACTGTCCAAG ACTGCAACTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1 5 10 15
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20 25 30
Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys
35 40 45
Pro Asn Ser Ser Ile Val Tyr Glu Ser Asp His His Ile Leu His Leu
50 55 60
Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Thr Ser Arg Cys Trp
65 70 75 80
Val Ala Leu Thr Pro Thr Val Ala Ala Pro Ile Leu Ser Ala Pro Leu
85 90 95

Met Ser Val Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr Leu
100 105 110

Ser Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu Val
115 120 125

Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Val Gln Asp
130 135 140

Cys Asn Cys Ser Ile
145

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATGAGCACAC TTCCAAARCC CCRAAGAAAA ACCAAAGAA ATACTAACCG TCGCCCTATG	60
GACGTCAAGT TCCCGGGCGG CGGCCAGATC GTTGGTGGAG TTTACTTGTT GCCGGGCAGG	120
GGCCCTCGTT TGGGTGTGCG CGCGACGAGA AAGACCTCCG AACGGTCCCA GCCTAGAGGC	180
AGGCCCCAGC CCATACCRAA GGTACGCCAG CCGACAGGCC GTAGCTGGGG TCAACCCGGC	240
TACCCTTGGC CCTTTATGG CAACGAGGGC TCGGGATGGG CGGGATGGCT CCTGTCCCCC	300
CGCGGGTCTC GTCTAATTG GGGCCCCAAC GACCCCGGC GAAGGTCCCG CAACTTGGGT	360
AAGGTCAATC ATACCTTAC ATNCGGNTA GCCGACCTCA TGGGTACAT CCTGTCTTA	420
GGAGGGCCGC TTGGCGGCGT TCGGGCTGCC CTGGCGCATG GCGTTAGGGC AATCGAGGAC	480
GGGTCAATT ACGCAACAGG GAATCTTCTT GGTGTCTCTT TTTCTACTT CCTCTTAGCA	540
CTGTTATCGT GCCTCACTAC ACCAGCTCA GCAATTCAAG TCAAGAACGC CTCTGGGATC	600
TACCATCTTA CCAATGACTG CTCGAACAAC AGCATCGTTT TTGAGGCGGA GACCATGATA	660
CTGCATCTTC CAGGTGTGTG CCCATGTATC AAGGCGGGGA ATGAGTCACG ATGTTGGCTC	720
CCTGTCTCCC CCACCTTAGC CGTCCCCAAC TCATCAGTGC CAATCCACGG GTTTCGCCGA	780
CACGTAGACC TCCTCGTTGG GGCAGCGGCA TTTTGTTCGG CCATGTACAT CGGAGACCTC	840
TGTGGTAGCA TAATCTTGCT AGGGCAGCTT TTTACTTTCA GGCCTAAGTA CCATCAGGTT	900
ACCCAGGATT GTAACGTCTC TATNAACNCT GGCCAAGTCA CGGGACACAG GATGGCA	957

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	1 5 10 15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	20 25 30

Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala
35						40			45						
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
50						55			60						
Ile	Pro	Lys	Val	Arg	Gln	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly
65			70						75			80			
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp
			85						90			95			
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro
			100						105			110			
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Xaa
115						120						125			
Xaa	Leu	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Leu	Gly	Gly	Pro	Leu
130						135						140			
Gly	Gly	Val	Ala	Ala	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Ile	Glu	Asp
145			150						155			160			
Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile
			165						170			175			
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Thr	Pro	Ala	Ser	Ala	Ile
			180						185			190			
Gln	Val	Lys	Asn	Ala	Ser	Gly	Ile	Tyr	His	Leu	Thr	Asn	Asp	Cys	Ser
195						200						205			
Asn	Asn	Ser	Ile	Val	Phe	Glu	Ala	Glu	Thr	Met	Ile	Leu	His	Leu	Pro
210						215						220			
Gly	Cys	Val	Pro	Cys	Ile	Lys	Ala	Gly	Asn	Glu	Ser	Arg	Cys	Trp	Leu
225			230						235			240			
Pro	Val	Ser	Pro	Thr	Leu	Ala	Val	Pro	Asn	Ser	Ser	Val	Pro	Ile	His
			245						250			255			
Gly	Phe	Arg	Arg	His	Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys
			260						265			270			
Ser	Ala	Met	Tyr	Ile	Gly	Asp	Leu	Cys	Gly	Ser	Ile	Ile	Leu	Val	Gly
275						280						285			
Gln	Leu	Phe	Thr	Phe	Arg	Pro	Lys	Tyr	His	Gln	Val	Thr	Gln	Asp	Cys
290						295						300			
Asn	Cys	Ser	Xaa	Asn	Xaa	Gly	His	Val	Thr	Gly	His	Arg	Met	Ala	
305			310						315						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGAGCACAC	TTCCAAAACC	CGAAAGAAAA	ACCAAAAGAA	ACACAAATCCG	CCGCCACAG	60
GACGTCAAAGT	TCCCGGGTGG	CGGCAGATC	GTTGGTGGAG	TCTACTTGCT	GCCGCAGG	120
GGCCCGCGCT	TGGGTGTGCG	CGCAGCAGA	AAGACTTCTG	AACGGTCCCA	GCCCAGAGGT	180
AGGCGCCAAC	CAATACCCAA	AGTGCACCAC	CAACGGGCC	GTACCTGGGC	CCAGCCCGGG	240

055138-050901

TACCCCTGGC CTCTTTATGG AAATGAGGGC TGTGGTTGGG CAGGCTGGCT CCTGTCCCC 300
CGCGGCTCTC GCCCAAATTG GGGCCCAAAC GACCCCCGGC GGAGGTCCCG CAACTTGGGT 360
AAGTCATCG ACACCCCTAC TTGCGGCTTC GCCGACCTCA TGGGGTATAT CCCTGTCGTA 420
GGCGCTCCGW TGGGAGGCGT CGCGGNGGCC TTGGCGCATG GGGTCANGN CATCGAGGAC 480
GGNGTAAATT ACGCAACAGN GAATCTTCCC GGNNGCTCTN TCTCTAICTT NCTCTGGCA 540
CTTCTCTCGT GCCTTACAAC ACCAGCCTCC GCGGCGCATT ATACCAACAA GTCTGGCCTG 600
TACCATCTCA CCRACGACTG CCCCAACAGC AGCATCGTTT ATGAGGCGGA GACACTGATT 660
TTGCACTTGC CTGGGTGTGT ACCTTGTGTG AAGRTGRACA ATCAATCCCG GTGCTGGGTG 720
CAGGCTCCCG CGACCTGGC AGTGCCGAAC GCGTCTACGC CAGTCACCGG GTTCCGCAAA 780
CATGTGGACA TCATGGTGGG CGCTGCCCGG TTCTGTTTCA CTATGTATGT GGGGGACCTG 840
TGGGGGGGCC TTTTCTCTGT TGGACAGCTC TTCACGCTCA GGCCTCGGAT GCATCAGGTT 900
GTCCAGGAGT GTAACGTTC CATCTACACA GGGCATATCA CTGGACACCG AATGGCA 957

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Ile
1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60
Ile Pro Lys Val Arg His Gln Thr Gly Arg Thr Trp Ala Gln Pro Gly
65 70 75 80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95
Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Xaa
130 135 140
Gly Gly Val Ala Xaa Ala Leu Ala His Gly Val Xaa Xaa Ile Glu Asp
145 150 155 160
Xaa Val Asn Tyr Ala Thr Xaa Asn Leu Pro Xaa Xaa Ser Xaa Ser Ile
165 170 175
Xaa Leu Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Ala
180 185 190
His Tyr Thr Asn Lys Ser Gly Leu Tyr His Leu Thr Asn Asp Cys Pro
195 200 205
Asn Ser Ser Ile Val Tyr Gly Ala Glu Thr Leu Ile Leu His Leu Pro
210 215 220
Gly Cys Val Pro Cys Val Lys Xaa Xaa Asn Gln Ser Arg Cys Trp Val

093156-0507

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

(2) INFORMATION FOR SEQ ID NO: 46:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Leu Leu Ser Pro Xaa Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro

0051138.050901

50 55 60
Ile Pro Lys Val Arg Gln Asn Gln Gly Arg Thr Trp Ala Gln Pro Gly
65 70 75 80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
85 90 95
Leu Leu Ser Pro Arg Gly Ser Arg Pro Asp Trp Xaa Pro Asn Asp Pro
100 105 110
Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 125
Gly Phe Ala Asp Leu Met Glu Tyr Ile Pro Val Val Gly Ala Pro Leu
130 135 140
Gly Gly Val Ala Ala Glu Leu Xaa His Gly Val Arg Ala Ile Glu Asp
145 150 155 160
Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175
Phe Xaa Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Leu
180 185 190
Asn Tyr Ala Asn Lys Ser Gly Leu Tyr His Leu Thr Asn Asp Cys Pro
195 200 205
Asn Ser Ser Ile Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu Pro
210 215 220
Gly Cys Val Pro Cys Val Lys Thr Gly Asn Leu Thr Lys Cys Trp Leu
225 230 235 240
Ser Ala Ser Pro Thr Leu Ala Val Gln Asn Ala Ser Val Ser Ile Arg
245 250 255
Gly Val Arg Glu His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys
260 265 270
Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu Val Gly
275 280 285
Gln Leu Phe Thr Phe Arg Pro Arg Met Tyr Glu Ile Ala Gln Asp Cys
290 295 300
Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met Ala
305 310 315

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATGAGCACAC TTCCTAAACC ACAAGAAAA ACCAAAAGAA ACACCAACCC CGGCCACAGG 60
ACGTTAAGTT CCCAGGCGGC GGTGAGATCG TTGGTGGAGT TIACGTGCTA CCACGCAGGG 120
GCCCCAGTT GGGTGTGCGT GCAGTGGCA AGACTTCGA GCGGTGCGAA CCTCGCAGTA 180
GGCGCCAACC CATCCCCAGG GCGCGCGGAA CCGAGGGCAG GTCTCTGGGCT CAGCCCGGGT 240
ACCTTGGCC CCTATATGGG AATCAGGGCT GCGGGTGGGC AGGGTGGCTC CTGTCCCGC 300
GCGGCTCTC 309

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1 5 10 15
 Asn Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
 20 25 30
 Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Gln Leu Gly Val Arg Ala
 35 40 45
 Val Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Ser Arg Arg Gln Pro
 50 55 60
 Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly
 65 70 75 80
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp
 85 90 95
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg
 115

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GACGGAATTA ATTTCGCAAC AGGGAATTTA CCTGGTTCCT CTTCTCTAT CTTCCTCTG 60
 GCTTTGTCT CATGCTTCT TACACCCACA GCCGGGCTGG AGTACCGTAA TGCCTCCGGA 120
 CTCTACATGG TAACTAACGA CTGCAGTAAC GGTAGTATCG TGTATGAGGC CGGGGATATT 180
 ATCCTCCACT TACCTGGCTG TGTCCCTGCG GTACGCTCTG GCAATACATC AAGATGCTGG 240
 ATCCCTGTGA GCCCYACCGT CGCCGTGAAG TCGCCCTGCG CCGCCACCGC CTCCTCCGC 300
 ACGCACGTGG ATATGATGGT GGGGCGGCCC ACCCTATGCT CAGCTCTCTA CGTAGGAGAC 360
 CTTTGTGGAG CGCTATTCT TGTGCGGCG GGGTCTCAT GGAGACATCG CCAGCATTTG 420
 ACTGTCCAGG ACTGCAACTG TTCCATC 447

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
 1 5 10 15
 Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Leu Thr Pro Thr Ala Gly
 20 25 30
 Leu Glu Tyr Arg Asn Ala Ser Gly Leu Tyr Met Val Thr Asn Asp Cys
 35 40 45
 Ser Asn Gly Ser Ile Val Tyr Glu Ala Gly Asp Ile Ile Leu His Leu
 50 55 60
 Pro Gly Cys Val Pro Cys Val Arg Ser Gly Asn Thr Ser Arg Cys Trp
 65 70 75 80
 Ile Pro Val Ser Xaa Thr Val Ala Val Lys Ser Pro Cys Ala Ala Thr
 85 90 95
 Ala Ser Leu Arg Thr His Val Asp Met Met Val Xaa Ala Ala Thr Leu
 100 105 110
 Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ala Leu Phe Leu Xaa
 115 120 125
 Gly Gln Gly Phe Ser Trp Arg His Arg Gln His Trp Thr Val Gln Asp
 130 135 140
 Cys Asn Cys Ser Ile
 145

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CTCGACACTT ACTGAGAATG ACATCCGTGT CGAGGAATCA ATATACCAAT GTTGTGACTT 60
 GGCCCCCGAG GCTCGCAAGG CCATAAGTC GCTCACCAG CGGCTGTACA TCGGGGGCCC 120
 YCTAACCAAT TCAAAGGAC AGAACTGCGG CTACCGTGGG TGCCGCGCCA GCGGCGTGCT 180
 GACTACCAGC TCGGCAACA CCCTGACATG CTACTTGAAA GCCAGAGCGG CCTGTGAGGC 240
 TGCAAAGCTC CGGACTGCA CCATGCTCGT GTGCGGGGAT GACCTTGTCG TTATCTGTGA 300
 GAGTGCGGGA GTCGAGGAAG ACGCGGCGAA CCTACGAGCT 340

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
 1 5 10 15
 Cys Cys Asp Leu Ala Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
 20 25 30

Glu Arg Leu Tyr Ile Gly Gly Xaa Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Ala Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CTGACAGTT ACTGAGAAGC ACATCCCTAC CGAGGRATCA ATCTATCAAT GTTGTGACTT 60
GGCCCCYGAG GCGCCGAAGG CCATAAAGTC GCTCACCAGAG CGGCTGTACG TCGGGGGCCCC 120
CCTAACCAAT TCAAAGGGGC AGAACTGCGG CTATCGTCGG TGTGCGGCTA GCGGCCTGCT 180
GACCAACGAGC TGCAGCAACA CCCTCACATG CTACTTGAAA GCCAGGGGGG CCTGTGAGGC 240
TGCAAAGCTC CAGGACTGCA CGATGCTCGT GTGCGGAGAC GACCTGTGCG TTATCTGTGA 300
GAGCGCGGGA GTCGAGGAGG ACGCGGCGAA CCTACGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Ser Thr Val Thr Glu Asn Asp Ile Arg Thr Glu Xaa Ser Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Ala Xaa Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Cys Glu Ser Ala Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100 105 110

[illegible]

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

(2) INFORMATION FOR SEQ ID NO: 58:

(ii) MOLECULE TYPE: peptide

```

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1      5      10      15
Cys Cys Asp Leu Ala Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20     25     30
Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35     40     45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50     55     60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65     70     75     80
Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85     90     95
Val Ile Cys Glu Ser Xaa Gly Val Glu Asp Ala Ala Asn Leu Arg
100    105    110

```

(2) INFORMATION FOR SEQ ID NO: 59A

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

069318

[illegible]

0695130

[illegible]

0695130

[illegible][illegible]

0695130

[illegible]

0695130

[illegible][illegible][illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CTCAACGGTC ACTGAAGCTG ATATCCGAAC AGAGGAGTCC ATATACCAAT GCTGTGACCT	60
GCACCCCGAA GCACGTGTAG CCATCAAGTC TTTGACTGAA AGGCTGTACG TCGGGGGGCC	120
CTTGACCAAT TCRAAAGGGG AGAACTGCGG CTATCGCAGA TGCCGTGCCA GCGGCGTCTT	180
GACAACCAGC TGCGGCAACA CCTCACCTG CTATATCAAG GCCCTAGCAG CCTGTAGAGC	240
TGCCAAGCTC CAGGACTGCA CCATGCTCGT CTGTGGCGAC GACCTGGTCG TGATCTGCGA	300
GAGTGTAGGG ACCCAGGAGG ATGCGGCGAG CCTGCGAGCC	340

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ser Thr Val Thr Glu Ala Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln	1 5 10 15
Cys Cys Asp Leu His Pro Glu Ala Arg Val Ala Ile Lys Ser Leu Thr	20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Glu Asn	35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys	50 55 60
Gly Asn Thr Leu Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Arg Ala	65 70 75 80
Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val	85 90 95
Val Ile Cys Glu Ser Val Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg	100 105 110
Ala	

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

NTCAACAGTC ACTGAGAGTG ATATCCGTAC AGAGGAGTCC ATCTACCAAT GCTGTGATCT	60
AGACCCCGAG GCTCGCAAGG CCATAAGGTC CCTCACAGAG AGGCTTTATA TCGGGGGTCC	120
CCTGACAAAC TCAAAAGGGC AGAACTGCGG CTACCGCCGA TGCCGTGCAA GCGGCGTCTT	180
GACGACTAGC TGCGGCAACA CCTCACCTG TTACATAAAG GCCAGGGCAG CCTGTGAGGC	240
TGCGAAGCTC CAGGATTGCT CAATGCTCGT CTGTGGCGAC GACCTGTGCG TTATCTGCGA	300
GATCGAGGGG NTCCANGAGG ATCCGTCGAN NNNNNNNNNN	340

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

Ser Thr Val Thr Glu Ser Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1      5      10      15
Cys Cys Asp Leu Asp Pro Glu Ala Arg Lys Ala Ile Arg Ser Leu Thr
20      25      30
Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35      40      45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50      55      60
Gly Asn Thr Leu Thr Cys Tyr Ile Lys Ala Arg Ala Ala Cys Arg Ala
65      70      75      80
Ala Lys Leu Gln Asp Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
85      90      95
Val Ile Cys Glu Ile Glu Gly Xaa Xaa Glu Asp Pro Ser Xaa Xaa Xaa
100      105      110
Xaa

```

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

CGTAGACCGT	GCACCATGAG	CACGAATCCT	AAACCTCAAA	GAAAACCAA	ACGTAACATC	60
AACCGCCGCC	CACAGGACGT	CAAGTTCCCG	GGCGGTGGCC	AGATCGTCGG	TGGAGTTTAC	120
CTGTTGCCCG	GCAGGGGCCC	TAGATTGGGT	GTCCGCGCGA	CTAGGAAGAC	TTCCGAGCGG	180
TCGCAACCTC	GTGGAGAGCG	ACAGCCTATC	CCCAAGGCTC	GCCGATCCGA	GGGCAGGTCC	240
TGGGCTCAGC	CCGGGTACCC	TTGGCCCTTC	TATGGCAATG	AGGGCATGGG	TTGGGCAGGG	300
TGGCTCCTGT	CCCCCATG	CTCCCGSCTT	AGTTGGGGCC	CTTCAGACCC	CCGGCCTAGG	360
TCGCGTAATT	TGGGTAAAGT	CATCGATACC	CTCACATCGG	GCTTCGCGCA	CCTCATGGGG	420
TACATTCCGC	TCGTCCGGCG	CCCCCTAGGG	GGCGTTGCCA	GGGCCCTTGC	GCAAGGCTTC	480
CGGGATCTAC	CACGTCACCA	AGCATTGTTT	CAATGGGAGC	ATTGTGTATG	AGGCGGAAGG	540
CATGATCATG	CATCTCCCGG	GGTGCGTGCC	CTGCGTTCGG	GAAGGTAATA	TCTCTCGTTG	600
CTGGGTACCG	TTTTCCCCCA	CGCTCGCAGC	CAGGAATGCT	ACCGTCCCCA	CTCAGGCAAT	660
TCGGCGACAC	GTCGACTTGC	TTGTTGGGGC	GGCCACACTC	TGTTCTGCTA	TGATGTGGG	720
GGACCTCTGT	GGGTCCGTCT	TCCTCGTCGG	CCAACTGTTT	ACCTTCACAW	CCCCCCAGNA	780
CTACACAGTG	CAAGACTGCA	ATTGTTCCAT	CTACCCCGGC	CATATAACGG	G	831

(2) INFORMATION FOR SEO ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Ile	Asn
1			5						10					15	
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
		20						25					30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala
	35						40					45			
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
	50					55					60				
Ile	Pro	Lys	Ala	Arg	Arg	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly
65					70					75					80
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp
				85					90					95	
Leu	Leu	Ser	Pro	His	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Ser	Asp	Pro
			100					105					110		
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys
		115					120					125			
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu
	130					135					140				
Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	Gln	Gly	Phe	Arg	Asp	Leu		
145				150					155						

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

NNNNNNNGTC	ACTGAGGTG	ATATCCGTGT	CGAGGARTCA	ATTTACCAAT	GCTGTGACCT	60
GGCCCCCGAG	GCTCGCGTAG	CCATAAAGTC	GCTCACTGAG	CGGCTATATG	TCGGGGGGCC	120
TCTCACCAAC	TCAAAGGAC	AGAACTGCGG	CTATCGCGCG	TGCCGTGCGA	GCGGTGTGCT	180
GACTACTAGC	TGCGGTAACA	CCCTCACATG	CTACCTGAAA	GCCGCCCGGG	CCTGTGAGGC	240
TGCAAAGCTC	CSGGAATGCA	CAATGCTCGT	GTGTGGCGAC	GACCTCGTCG	TTATCTGTGA	300
GAGTGGGGGG	GTCCAGGAGG	ATGCTGCAAG	CCTNNNNNNN			340

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Xaa Xaa Val Thr Glu Ser Asp Ile Arg Val Glu Xaa Ser Ile Tyr Gln
1 5 10 15
Cys Cys Asp Leu Ala Pro Glu Ala Arg Val Ala Ile Lys Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50 55 60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ala Ala Cys Arg Ala
65 70 75 80
Ala Lys Leu Arg Glu Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Cys Glu Ser Ala Gly Val Gln Glu Asp Ala Ala Ser Xaa Xaa
100 105 110
Xaa

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CTCGACAGTC ACAGAGAGAG ATATAAGNAC TGAGGAGTCC ATATACORGG CTGTTCCTT 60
ACCCGAGCAG GCCAGAACTG CCATACACTC ATTGACTGAG AGACTCTACG TAGGAGGGCC 120
CATGATGAAC AGCAAAAGGC AATCCTCGCG ATACAGGCAT TGCCGCGCCA GCGGAGTGCT 180
CACCACCACT ATGGGGAATA CCATCACGTG CTACATCAAG GCCCTAGCGG CTGTGAAGC 240
AGCAGGAATA GTGCCGCCCA CCATGCTGCT GTCCGCGCAT GACCTAGTIG TCATCTCAGA 300
GAGTCAGGGA GTCGAGGAGG ACGACCGGAA CCTGANNNNN 340

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ser Thr Val Thr Glu Arg Asp Ile Xaa Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
35 40 45
Cys Gly Tyr Arg His Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met

50 55 60
 Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala
 65 70 75 80
 Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ser Glu Ser Gln Gly Val Glu Glu Asp Asp Arg Asn Leu Xaa
 100 105 110
 Xaa

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTCAACCGTC ACAGAGAGGG ATATAAGAAC TGAGGAGTCC ATATACCTGG CCTGCTCCTT 60
 ACCCGAGCAG GCCCGGACTG CCATACATTC ATTAAGTGG AGACTTTACG TGGGAGGGCC 120
 CATGATGAAC AGCAAAGGGC AGTCCTGCGG ATACAGGCGT TGCCGCGCTA GCGGAGTGCT 180
 CACCACCACT ATGGGGAACA CCATCAGCTG TTATGTGAAA GCCCTCGCAG CTTGTAAAGC 240
 TGGGGGCATT GTTGCCCCCA CGATGCTGGT GTGCGGCGAT GACCTGGTTG TCATCTCAGA 300
 GAGTCAGGGG GCTGAGGAGG ACGAGCGAAA CCTGAGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
 1 5 10 15
 Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
 20 25 30
 Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
 35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
 50 55 60
 Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala
 65 70 75 80
 Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Ile Ser Glu Ser Gln Gly Ala Glu Glu Asp Glu Arg Asn Leu Arg
 100 105 110
 Val

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CTCAACAGTC GCGGAGAGAG ACATCAGGAC CGAGGAGTCC ATTTACCTTG CCTGCTCCTT	60
ACCCGAGCAA GCCCGAACTG CCATACATTC ATTGACTGAG AGACTTTACG TAGGAGGGCC	120
CATGATGAAC AGCAAGGGAC AGTCCTCGG TTACAGACGT TGCCGCGCCA GCGGAGTGCT	180
CACCACCAGC ATGGGGGAATA CCATCACATG CTATGTGAAG GCATTAGCTG CCTGCAAAGC	240
TGCAGGCATC GTTGCTCCCA CGATGCTGGT TTGTGGCGAC GATCTGGTCA TCATCTCAGA	300
GAGTCAGGGA ACCGAGGAGG ATGAGCGGAA CCTGAGAGTC	340

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Ser Thr Val Ala Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu	1	5	10	15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr	20	25	30	
Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser	35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met	50	55	60	
Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala	65	70	75	80
Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val	85	90	95	
Ile Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg	100	105	110	
Val				

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CGNACANCT CCAGGCCCCC CCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG 60
TACACCGGAA TTGCCCCGAA GACTGGGTCC TTTCTTGGAT AAACCCACTC TATGCCCGGC 120
CATTGCGCGG TGCCCCGCA AGACTGCTAR CCGAGTAGCG TTGGGTGCG AAAGGCCCTG 180
TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCAGGAGG TCTCGTAGAC CGTGCTCAT 240
GAGCACAAAT CCTAAACCTC AAAGAAAAAC CAAAAGAAAC ACTAACCGCC GCCCACAGGA 300
CGTTAAGTTC CCGGGCGGTG GCCAGATCGT TGGCGGAGTA TACTTGTTGC CNTGCAGGGG 360
NCCCAGGTNG NGTNTATGCG CAACGANGAA GACTNCCGAA CAGTCCCAGC CACGTGGGAG 420
GGCCAGCCCC ATCCCGAAG ATCGGNGCAC CACTGGCAAG TCCTGGGGAC GTCCAGGATA 480
TCCCTGGCCC CTGTATGGGA ACGAGGGCCT CGGTGGGCA GGGTGGCTCC TGTCCCCCG 540
GGCTCCCGC CGTTCATGGG CCCCCACGGA CCCCAGGAT AGGTCCGCGCA ACTTGGGTAA 600
GGTCATCGAT ACCCTCACGT NCGGCTTTNC CGACCTCATG GGGTACATTC CCGTCGTGG 660
CCCCCAGTA GNGGCGTCC CCAGAGCTCT CGCGCATGGC GTGAGAGTCC TGGAGGACGG 720
GATAAACTAT GAACAGGGA ACCTCCCCGG TTGCTCTTTC TCTATCTCCC TCCTTGCTCT 780
TCTGTCTGA ATTACCGNCC CAGTTTCTGC TGTGGAAATC AAAACACCA GMAACACATA 840
CATGGTGACT AACGACTGTT CAACAGYAG CATCACCTGG CAGCTTNGN NCGCGGTGCT 900
TCACGTTCTT GGATGCTCC CTTGTGAACG AGAGGGCAAC AGTCCCGGT GCTGGATTCC 960
AGTCACGCCC RACGTAKNCG TGAGCCGACC TGGTGGCCTA ACCGAGGGTT TGGATCGCA 1020
CATCGACACC ATCTAGCGT CCGCAACATT TTGTTCTGCC CTCTACATAG GGGATGATG 1080
TGGCGCGATA ATGATAGCTG CCCAAGTGGT CATCGTCTCG CCGGAGCATC ATCATTGT 1140
CCAGGACTGT AACTGTTCCA TCTACCGGG CCACATAACG GGGCTCGTA TGNG 1195

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30
Gly Val Tyr Leu Leu Xaa Cys Arg Xaa Pro Arg Xaa Xaa Xaa Cys Ala
35 40 45
Thr Xaa Lys Thr Xaa Glu Gln Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60
Ile Pro Lys Asp Arg Xaa Thr Thr Gly Lys Ser Trp Gly Arg Pro Gly
65 70 75 80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
85 90 95
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100 105 110
Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Xaa
115 120 125
Gly Phe Xaa Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
130 135 140

Xaa Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145 150 155 160

Gly Ile Asn Tyr Glu Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
165 170 175

Ser Leu Leu Ala Leu Leu Ser Ile Thr Xaa Pro Val Ser Ala Val Glu
180 185 190

Ile Lys Asn Thr Xaa Asn Thr Tyr Met Val Thr Asn Asp Cys Ser Asn
195 200 205

Xaa Ser Ile Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val Pro Gly
210 215 220

Cys Val Pro Cys Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro
225 230 235 240

Val Thr Pro Xaa Val Xaa Val Ser Arg Pro Gly Ala Leu Thr Glu Gly
245 250 255

Leu Arg Ser His Ile Asp Thr Ile Val Ala Ser Ala Thr Phe Cys Ser
260 265 270

Ala Leu Tyr Ile Gly Asp Val Cys Gly Ala Ile Met Ile Ala Ala Gln
275 280 285

Val Val Ile Val Ser Pro Glu His His His Phe Val Gln Asp Cys Asn
290 295 300

Cys Ser Ile Tyr Pro Gly His Ile Thr Gly Pro Arg Met Xaa
305 310 315

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

ATCCACAGTC ACTGAAAGAG ACATCAGAGT TGAAGAGTCC GTTTATCTGT CCTGTTCACT 60

TCCCGAGGAG GCCCGAGCTG CCATACACTC ACTAACTGAG AGGCTGTACG TGGGAGGTCC 120

CATGCAGAAC AGCAAGGGGC AATCCTGCGG ATACAGGCGC TGCCGCGCCA GCGGGGTGCT 180

CACCACTAGC ATGGGGAATA CTCTCACATG CTACTTGAAG GCCCAGGCGG CCTGCAGGGC 240

CGCGGGCATT GTTGACCCCA CAATGCTGGT GTGTGGCGAC GACCTGGTCG TCATCTCAGA 300

GAGTCAGGGG ACTCAGAGGG ACGAGAACAA CCTGAGACCT 340

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Ser Val Tyr Leu
1 5 10 15

Ser Cys Ser Leu Pro Glu Glu Ala Arg Ala Ala Ile His Ser Leu Thr
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Gln Asn Ser Lys Gly Gln Ser
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
50 55 60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65 70 75 80
Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ser Glu Ser Gln Gly Thr Glu Arg Asp Glu Asn Asn Leu Arg
100 105 110
Pro

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

CTCAACAGTC ACGGAGAGGG ACATCAGGAA TGAGGAGTCC ATATTCCTGG CCTGCTCGTT 60
GCCCCGAGGAG GCCCCGAGTC TCATACATTC GCTCACTGAG AGACTCTACA TAGGCCGGCC 120
GATGATGAAC AGCAAAGGCC AGTCCTGTGG ATACAGGCGT TGTCGCGCCA GCGGGGTGTT 180
CACCCTAGC ATGGGCAATA CCATCACGTG CTATGTGAAA GCCATGGCAG CTTCGAGAGC 240
TGCCGGGATT GACGCCCCCA CAATGTTGGT ATGTGGCGAC GACCTGGTGG TCATCTCAGA 300
GAGTCAGGGG ACCGAGGAGG ACCAGCGAAA TCTGAGAGTC 340

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ser Thr Val Thr Glu Arg Asp Ile Arg Asn Glu Glu Ser Ile Phe Leu
1 5 10 15
Ala Cys Ser Leu Pro Glu Glu Ala Arg Thr Val Ile His Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Ile Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
50 55 60
Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Met Ala Ala Cys Arg Ala
65 70 75 80
Ala Gly Ile Asp Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

```

CTCTTGACTC TACTGTCACT GAACAGGATA TCAGGGTAGA AGAAGAAATA TACCAATGTT    60
GTGACCTTGA GCCGGAGGCT AGACGGGCCAA TCAATCGCT CACGGAACGG CTTTACGTTG    120
GAGGTCCCAT GTTCAACAGC AAGGGGCTCA AATGCGGATA TCGCCGTTGC CGTGCTAGCG    180
GTGTATTGCC CACTAGCTAC GGTAAATACAA TCACCTGCTA CATCAAGGCC AGAGCGGCTG    240
CTCGAGCTGC GGGCCTTCAA GACCCATCAT TCCTTGCTG CCGAGAIGAT TTGGTGGTAG    300
TGGCTGAGAG TTGCGKCGTT GATGAGGAGG ATAGGGCAGC                            340

```

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
1           5           10           15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Lys Ser Leu Thr
20          25          30
Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Leu Lys
35          40          45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Tyr
50          55          60
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Arg Ala Ala Arg Ala
65          70          75          80
Ala Gly Leu Gln Asp Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
85          90          95
Val Val Ala Glu Ser Cys Xaa Val Asp Glu Glu Asp Arg Ala Ala Leu
100         105         110

```

Arg

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CTCCACTGTA ACCGAAAAGG ACATCAGGCC CGAGGAAGAG GTCTATCAGT GTTGTGACCT 60
GGAGCCCGAA GCTCGCAAGG TTATTACCGC CCTCACAGAA AGACTCTACG TGGGCGGCCC 120
CATGCACAAC AGCAAGGGAG ACCTTTGTGG GTATCGGAGA TGCCGCGCAA GCGGCGTCTA 180
CACGACCAGC TTCGGAAACA CACTGACGTG CTACCTCAAA GCCTCAGCTG CTATTAGAGC 240
GGCAGGGCTG AGAGACTGCA CCATGCTGGT TTGCGGTGAC GACTTGGTCG TCATCGCTGA 300
GAGCGATGGC GTAGAGGAGG ATAACCGAGC CCTCCNAGCC 340

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Ser Thr Val Thr Glu Lys Asp Ile Arg Pro Glu Glu Glu Val Tyr Gln
1 5 10 15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
50 55 60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
65 70 75 80
Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Asn Arg Ala Leu Xaa
100 105 110
Ala

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CTCCACGGTG ACTGAAAAGG ACATCAGGGT CGAGGAAGAG ATCTATCAAT GTTGTGACCT 60
GGARCCCGAA GCCCGCAAAG CAATATCCGC CCTCACAGAG AGRCTCTACT TGGGCGGCCC 120
CATGTATAAC AGCAAAGGGG AGCTCTGCGG GTATCGGAGG TGCCGCGCGA GCGGAGTGTA 180
CACCACAAGT TTCGGGAACA CAGTGACCTG CTATCTTAAG GCCACCGCAG CTACCAGGGC 240
TGCAGGCCTA AAAGACTGCA CCATGCTGGT CTGCGGTGAC GACTTGGTCG TCATCGCCGA 300

09651138.050901

GAGCGAGGGC GTAGAGGAGG ATTCCCAACC CCTCCGAGCC

340

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
1 5 10 15
Cys Cys Asp Leu Xaa Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr
20 25 30
Glu Xaa Leu Tyr Leu Gly Gly Pro Met Tyr Asn Ser Lys Gly Glu Leu
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
50 55 60
Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala
65 70 75 80
Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Glu Gly Val Glu Glu Asp Ser Gln Pro Leu Arg
100 105 110
Ala

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTCCACCGTA ACCGAAAGGG ACATCAGGGT CGAGGAGGAG GTCTATCAGT GTTGTGATCT 60
GGAGCCAGAG GCCCGCAAGG CAATATCCGC CCTCAGGAG AGACTCTATG TGGGCGGTCC 120
CATGTTTAAC AGCAAGGGAG ACCTATGTGG CTACCGCAGG TGCCGCGCAA GCGGCGTCTA 180
CACCACCAGC TTCGGAACA CACTGACCTG CTACCTCAAG GCCACGGCCG CTACCAGAGC 240
GGCCGGCCTG AAGGATTGCA CAATGCTGGT TTGCGGGGAC GACCTGGTCG TCATCGCAGA 300
GAGCGATGGC GTGGACGAGG ACCGCCGAGC CCTCCAAGCT 340

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln

```

      1          5              10             15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr
        20                25                 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu
       35               40                45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
     50           55            60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala
    65         70         75         80
Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
      85           90           95
Val Ile Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Arg Ala Leu Gin
      100        105        110

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

(2) INFORMATION FOR SEQ ID NO: 90;

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ser Thr Val Thr Glu Arg Asp Val Gln Thr Glu His Asp Ile Tyr Gln
 1 5 10 15
 Cys Cys Lys Leu Glu Pro Ala Ala Arg Thr Ala Ile Thr Ser Leu Thr
 20 25 30
 Asp Arg Leu Tyr Xaa Gly Gly Pro Met Xaa Asn Ser Lys Gly Gln Ala
 35 40 45
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ile Leu
 50 55 60
 Ala Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
 65 70 75 80
 Ala Gly Leu Lys Asp Phe Asp Met Leu Val Cys Gly Asp Asp Leu Val

050901

(2) INFORMATION FOR SEQ ID NO: 91:

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Alo

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```
CTCTCCGTC ACGGAGCGTG ACATCCGCAC TGAACACGAC ATCTATCAGT GCTGCCAATT    60
AGATCCGGTA GCACGGAAAG CCATTACATC TCTTACTGAG CGGCTGTACT GCGGCGGGCC    120
CATGTACAAC TCTCGAGGTC AGTCATGTGG GTACCGCAGG TGCCGGGCTA GTGGTGTCTT    180
CACCACAAGC TTGGGCAACA CCATGACATG CTACCTGAAG GCTCAGGCGG CTTGTAGGGC    240
AGCRAAGCTC AAAAACTTTG ACATGTTGGT CTGCGGAGAC GACCTAGTCG TTATTGCTGA    300
GAGCGGAGGA GTCCCTGAGG ATGCCGGGGC CCTGCGAGTC    340
```

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```
Ser Ser Val Thr Glu Arg Asp Ile Arg Thr Glu His Asp Ile Tyr Gln
1           5           10           15
Cys Cys Gln Leu Asp Pro Val Ala Arg Lys Ala Ile Thr Ser Leu Thr
20          25          30
Glu Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Arg Gly Gln Ser
35          40          45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50          55          60
Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala
65          70          75          80
Xaa Lys Leu Lys Asn Phe Asp Met Leu Val Cys Gly Asp Asp Leu Val
85          90          95
Val Ile Ala Glu Ser Gly Gly Val Pro Glu Asp Ala Gly Ala Leu Arg
100         105         110
Val
```

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```
ATCCACAGTC ACGGGGCGCG ACATACGCAC AGAACNAGAC ATTTACCTGT CCTGCCAGCT    60
CGACCCAGAG GCGCGGAAAG CCATAAAGTC TCTCACTGAG AGGCTCTATG TCGGGGGCCC    120
TATGTACAAC TCAAAGGGCC AACTCTGTGG TCAACGCCGA TGCCGAGCAA GCGGAGTACT    180
```

CCCCACAAGC ATGGGTAACA CCATCACATG CTTCTGAAG GCAACCGCCG CTGCGGAGC 240
 AGCCGGCTTT ACAGATTATG ACATGTTGGT CTGCGGAGAC GATTGGTTG TGTAACTGA 300
 GAGTGCTGGA GTCAACGAGG ATATCGCTAA CCTGCGAGCC 340

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Ser Thr Val Thr Gly Arg Asp Ile Arg Thr Glu Xaa Asp Ile Tyr Leu
 1 5 10 15
 Ser Cys Gln Leu Asp Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
 20 25 30
 Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Leu
 35 40 45
 Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Met
 50 55 60
 Gly Asn Thr Ile Thr Cys Phe Leu Lys Ala Thr Ala Ala Cys Arg Ala
 65 70 75 80
 Ala Gly Phe Thr Asp Tyr Asp Met Leu Val Cys Gly Asp Asp Leu Val
 85 90 95
 Val Val Thr Glu Ser Ala Gly Val Asn Glu Asp Ile Ala Asn Leu Arg
 100 105 110
 Ala

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CTCCACTGTC ACTGAGCAGG ACATCAGGGT AGAACTTTCC ATCTTCAGG CCTGTGACCT 60
 CAAGGACGAG GCTAGGAGGG TGATAACTTC ACTACGGAG CGGCTTTACT GTGGTGGTCC 120
 TATGTTCAAC AGCAAGGGAC AACACTGCCG TTACCGCCGC TGCCGTGCTA GTGGGGTGCT 180
 ACCCACCAGC TTCGGGAACA CAATCACCTG TTACATCAAA GCAAAGGCAG CTACCAAAGC 240
 TGCCGGAATT AAAAATCCAT CATTCTTGT CTGCGGAGAT GACTTGGTCG TGATTGCTGA 300
 GAGTGCAGGG ATCGATCAGG ACAAGACCGC CTTGAGACCT 340

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Leu Ser Ile Phe Gln
1 5 10 15
Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
50 55 60
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
65 70 75 80
Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Lys Ser Ala Leu Arg
100 105 110
Ala

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CTCTACCGTC ACAGAGAGGG ACATACGGAC AGAAGAATCC ATCTATCTGT CTGTCAATT 60
GCGTGAAGAG GCCCGGAAG CCATTAAATC GCTGACAGAG AGACTATACG TGGCGGCCCC 120
GATGGAAAAC AGCAAGGGCC AGGCTTGCGG ATATAGGCGT TGGCGCGCAA GCGGGGTATT 180
CACCACAAGC TTGGGGAACA CCATGACTTG TTACATCAAA GCTAAAGCGG CTGTAAAGC 240
CGCTGGCATT GTAGACCCGG TGATGCTCGT GTGCGGTGAC GACCTAGTGG TCATCTCAGA 300
AAGCAAGGGG GTGAGGAGG ACCAGCGGA CCTACGACTC 340

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
1 5 10 15
Ser Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Lys Ala Ala Cys Lys Ala
65 70 75 80
Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Arg
100 105 110
Val

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTCCACTGTC ACTGAGAGAG ACATACGAGC AGAAGAATCC ATCTAATYTTGG CTGTGCAATT 60
GCCCGAAGAG GCCCGGAAGG CCATTAAATC ACTGACAGAG AGACTATACG TGGGCGGCCC 120
GATGGAAAAC AGCAAAGGCC AGGCCTGCGG ATATAGGCGT TGCOCGCGAA GCGGGGTATT 180
CACCACAAGC TTGGGGAACA CCATGACTTG TTACATCAAG GCCAARGCAG CTGTAAAGC 240
YGCTGGCATT GTTGACCCGG TGAATGCTCGT GTGCGGCGAC GACCTAGTGG TCATCTCAGA 300
GAGCAAGGGG GTAGAGGAGG ACCAGCGAGA CCTAC 335

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Xaa Xaa
1 5 10 15
Ala Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50 55 60
Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Xaa Ala Ala Cys Lys Xaa
65 70 75 80
Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Xaa
100 105 110
Xaa

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```
CGTACAGCCT CCAGGACCCC CCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG    60
TACACCGGAA TTGCCGGGAA GACTGGGTCC TTTCTTGAT TAACCCACTC TATGCCCGGA    120
GATTTGGGCG TGCCCCCGCA AGACTGCTAG CCGAGTAGCG TTGGGTTCG AAAGGCCTTG    180
TGGTACTGCC TGATAGGGTG CTTCGAGTG CCCCAGGAGG TCTCGTAGAC CGTGACCATT    240
GAGCACGAAT CTAACCTC AAAGACAAAC CAAAAGAAAC ACCAACCACC GCCCACAGGA    300
CGTTAAGTTC CCGGGCGGTG GCCAGATCGT TGGCGGGGTG TACTTGTGTC CGCGCAGGGG    360
CCCCAGAGTG GGTGTGCGCG CGACGAGAAA GACCTCGGAG CGGTCCAGC CGCGTGGGAG    420
GCGCCAACTT ATCCCCAAGG TTAGGCGCAC CACCGGCGGT T                      461
```

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Gln Thr Lys Arg Asn Thr Asn
1          5          10          15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20          25          30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Val Gly Val Arg Ala
35          40          45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50          55          60
Ile Pro Lys Val Arg Arg Thr Thr Gly Arg
65          70
```

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```
CTCTACTGTC ACAGAGAGGG ATATACGAAC AGAGGAATCC ATYTATCTGG CTGTCAATT    60
GCCCCAAGAG GCCCCGAAGG CCATCAAATC ACTGACAGAG AGACTATACG TGGGCGGCCC    120
GATGGAAGAC AGCAAGGGCC AGGCCTGCGG ATACAGGCGT TGCCGCGCAA GCGGGGTATT    180
```

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FOUO

CACCACAAGC TTGGGGAACA CCATGACTTG TTACATCAA GCCAAGGCGG CTTGTAAAGC 240
CGCTGGCATT GTTGACCCAG TGATGCTCGT GTGCGGCGAC GACCTAGTGG TCATOTCAGA 300
AAGCAAGGGG GTGGAGGAGG ACCAACGAGA CCTACGANTC 340

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Xaa Tyr Leu
1 5 10 15
Ala Cys Gln Leu Pro Glu Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Glu Asn Ser Lys Gly Gln Ala
35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Leu
50 55 60
Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Lys Ala Ala Cys Lys Ala
65 70 75 80
Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95
Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Arg
100 105 110
Xaa

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ala Arg Gln Ser Asp Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

(2) INFORMATION FOR SEQ ID NO: 110:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

(2) INFORMATION FOR SEQ ID NO: 111:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

(2) INFORMATION FOR SEQ ID NO: 112:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

(2) INFORMATION FOR SEQ ID NO: 1/13:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

(2) INFORMATION FOR SEQ/ID NO: 114:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

050901

Val	Arg	Gln	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln
1				5					10	

1 5 10

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Val	Arg	His	Gln	Thr	Gly	Arg	Thr	Trp	Ala	Gln
1				5					10	

1 5 / 10

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val Arg Gln Asn Gln Gly Arg Thr Trp Ala Gln
1 5 10

1 5 10

(2) INFORMATION FOR SEQ ID NO: 117:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY; linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln
1 5 10

1 5 / 10

(2) INFORMATION FOR/ SEQ ID NO: 118:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

Val	Arg	Arg	Thr	Thr	Gly	Arg	Xaa	Xaa	Xaa	Xaa
1				5					10	

1 / 5 10

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Val Arg Arg Thr Thr Gly Arg Thr Trp Ala Gln
1 5 10

1 5 10

00651138 050901

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Tyr Glu Val His Ser Thr Thr Asp Gly Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Val Glu Val Lys Asn Thr Ser Gln Ala Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Ile Gln Val Lys Asn Asn Ser His Phe Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Val Gln Val Lys Asn Thr Ser Thr Met Tyr Met Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Gln Val Lys Asn Thr Ser His Ser Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Val Gln Val Ala Asn Arg Ser Gly Ser Tyr Met Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Val Glu Ile Lys Asn Thr Xaa Asn Thr Tyr Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val Glu Ile Lys Asn Thr Ser Asn Thr Tyr Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Ile Asn Tyr Arg Asn Val Ser Gly Ile Tyr Tyr Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ile Asn Tyr Arg Asn Thr Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 132:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Ile Asn Tyr His Asn Thr Ser Gly / Ile Tyr His Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Thr Asn Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Ile Gln Val Lys / Asn Ala Ser Gly Ile Tyr His Leu

1 5 10

(2) INFORMATION FOR SEQ ID NO: 136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Ala His Tyr Thr Asn Lys Ser Gly Leu Tyr His Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Leu Asn Tyr Ala Asn Lys Ser Gly Leu Tyr His Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Leu Glu Tyr Arg Asn Ala Ser Gly Leu Tyr Met Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Ile Tyr Glu Met Ser Gly Met Ile Leu His Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 141:

106050 SEPT 58

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Val Tyr Glu Ala Lys Asp Ile Ile Leu His Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

Val Trp Gln Leu Xaa Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

Val Trp Gln Leu Arg Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 144:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Ile Trp Gln Met Gln Gly Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

Val Trp Gln Leu Lys Asp Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:
Val Trp Gln Leu Glu Glu Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 147:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 148:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Val Tyr Glu Ala Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 149:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

Val Tyr Glu Ala Asp His His Ile Leu Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 150:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Val Phe Glu Ala Asp His His Ile Leu His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 151:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:
 Val Tyr Glu Ser Asp His His Ile Leu His Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Val Phe Glu Glu Thr Met Ile Leu His Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Val Tyr Glu Ala Glu Thr Leu Ile Leu His Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Val Tyr Glu Ala Gly Asp Ile Ile Leu His Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Val Arg Glu Asp Asn His Leu Arg Cys Trp Met Ala Leu
 1 5 10

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(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Met Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Ile Arg Glu Gly Asn Ile Ser Arg Cys Trp Val Leu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Glu Asn Ser Ser Gly Arg Phe His Cys Trp Ile Pro Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Glu Arg Ser Gly Asn Arg Thr Phe Cys Trp Thr Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Glu Leu Gln Gly Asn Lys Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 162:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Glu Arg His Gln Asn Gln Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Glu Trp Lys Asp Asn Thr Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Val Arg Glu Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

Val Arg Val Gly Asn Gln Ser Ser Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Val Lys Glu Gly Asn His Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Val Lys Thr Gly Asn Thr Ser Arg Cys Trp Val Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Ile Lys Ala Gly Asn Glu Ser Arg Cys Trp Leu Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

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Val Lys Xaa Xaa Asn Gln Ser Arg Cys Trp Val Gln Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Val Lys Thr Gly Asn Leu Thr Lys Cys Trp Leu Ser Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Val Arg Ser Gly Asn Thr Ser Arg Cys Trp Ile Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Val Lys Asn Ala Ser Val Pro Thr Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Val Lys Asp Ala Asn Val Pro Thr Ala Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

Ala Arg Ile Ala Asn Ala Pro Ile Asp Glu
1 5 10

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(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Val Ser Lys Pro Gly Ala Leu Thr Lys Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

Val Ser Arg Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Val Asn Gln Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Val Ser Gln Pro Gly Ala Leu Thr Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Val Ser Arg Pro Gly Ala Leu Thr Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Ala Pro Tyr Ile Gly Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Ala Pro Tyr Thr Ala Ala Pro Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Ala Pro Ile Leu Ser Ala Pro Leu Met Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Val Pro Asn Ser Ser Val Pro Ile His Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Val Pro Asn Ala Ser Thr Pro Val Thr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

Val Gln Asn Ala Ser Val Ser Ile Arg Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Val Lys Ser Pro Cys Ala Ala Thr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Ser Pro Arg Met His His Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Ser Pro Arg Leu Tyr His Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

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Thr Ser Arg Arg His Trp Thr Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Ala Pro Lys Arg His Tyr Phe Val Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Ser Pro Gln Tyr His Thr Phe Val Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Ser Pro Gln His His Asn Phe Ser Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Ser Pro Gln His His Ile Phe Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Ser Pro Glu His His His Phe Val Gln Asp
1 5 10

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(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Arg Pro Arg Arg His Trp Thr Ala Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Gln Pro Arg Arg His Trp Thr Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Arg Pro Arg Arg His Trp Thr Thr Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Gln Pro Arg Arg His Trp Thr Val Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

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- (3) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Arg Pro Lys Tyr His Gln Val Thr Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Arg Pro Arg Met His Gln Val Val Gln Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Arg Pro Arg Met Tyr Glu Ile Ala Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

Arg His Arg Gln His Trp Thr Val Gln Asp
1 5 10